

Figure 1

2588 GA TCAATCGCAT TCATTTAAG AAATTATAACC TTITTAGTAC TTGCTGAAGA
 2641 ATGATTCAAG GTAAATCACA TACTTGTT AGAGAGGCAG GGGGTTAAC CCGAGTCACC
 2701 CAGCTGGTCT CATACTAGA CAGCACTGT GAAGGATTGA ATGCAGGTTC CAGGTGGAGG
 2761 GAAGACGTGG ACACCATCTC CACTGAGCCA TGCAAGACATT TTTAAAAGCT ATACACAAAAA
 2821 TTGTGAGAAG ACATTGCCA ACTCTTCAA AGTCTTCTT TTTCCACGTG CTTCTTATT
 2881 TAAGCGAAAT ATATTGTTG TTTCTTCCTA AAAAAAAA 2890

Figure 2

1 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTATCTTCCTGATCCTGATC 60
 61 TCTGTTGGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATTTCAAATAAGCC 120
 121 ATGCCCTCTGCAGGAACACTTCCTGGGTTAGGGGATTATCTGTAATGCCAACACCC 180
 1 M P S A G T L P W V Q G I I C N A N N P 20
 181 TGTGTTCCGTTACCGACTCCTGGGGAGGCTCCGGAGTTGGAAACTTAACAAATCC 240
 21 C F R Y P T P G E A P G V V G N F N K S 40
 241 ATTGTGGCTCGCCTGTTCTCAGATGTCGGAGGCTTCTTATACAGCCAGAAAGACACC 300
 41 I V A R L F S D A R R L L L Y S Q K D T 60
 301 AGCATGAAGGACATGCGAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 360
 61 S M K D M R K V L R T L Q Q I K K S S S 80
 361 AACCTGAAGCTTCAAGATTCCCTGGTGGACAATGAAACCTCTCTGGGTTCTGTATCAC 420
 81 N L K L Q D F L V D N E T F S G F L Y H 100
 421 AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC 480
 101 N L S L P K S T V D K M L R A D V I L H 120
 481 AAGGTATTTGCAAGGCTACCAAGTTACATTGACAAGTCTGTGCAATGGATCAAAATCA 540
 121 K V F L Q G Y Q L H L T S L C N G S K S 140
 541 GAAGAGATGATTCAACTTGGTGACCAAGAAGTTCTGAGCTTGTGGCTACCAAGGGAG 600
 141 E E M I Q L G D Q E V S E L C G L P R E 160
 601 AAACTGGCTGCAGCAGAGCGAGTACTCGTTCAACATGGACATCCTGAAGCCAATCCTG 660
 161 K L A A A E R V L R S N M D I L K P I L 180
 661 AGAACACTAAACTCTACATCTCCCTCCCGAGCAAGGAGCTGGCGAAGCCACAAAACA 720
 181 R T L N S T S P F P S K E L A E A T K T 200
 721 TTGCTGCATAGTCTGGACTCTGGCCCAGGAGCTGTCAGCATGAGAAGCTGGAGTGAC 780
 201 L L H S L G T L A Q E L F S M R S W S D 220
 781 ATGCGACAGGAGGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCCACCCAAATC 840
 221 M R Q E V M F L T N V N S S S S S T Q I 240
 841 TACCAAGGCTGTCTCGTATTGTCTGCGGGCATCCGAGGGAGGGGGCTGAAGATCAAG 900
 241 Y Q A V S R I V C G H P E G G G L K I K 260
 901 TCTCTCAACTGGTATGAGGACAACAACAAAGCCCTCTTGGAGGCAATGGCACTGAG 960
 261 S L N W Y E D N N Y K A L F G G G N G T E 280

961 GAAGATGCTGAAACCTTCTATGACAACCTACAACCTACTGCAATGATTGATGAAG 1020
281 E D A E T F Y D N S T T P Y C N D L M K 300
1021 AATTGGAGTCTAGCCTCTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT 1080
301 N L E S S P L S R I I W K A L K P L L V 320
1081 GGGAAAGATCCTGTATAACACCTGACACTCCAGCCACAAGGCAGGTATGGCTGAGGTGAAC 1140
321 G K I L Y T P D T P A T R Q V M A E V N 340
1141 AAGACCTTCAGGAACCTGGCTGTGTTCCATGATCTGAAGGCATGTGGGAGGAACTCAGC 1200
341 K T F Q E L A V F H D L E G M W E E L S 360
1201 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG 1260
361 P K I W T F M E N S Q E M D L V R M L L 380
1261 GACAGCAGGGACAATGACCACCTTGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC 1320
381 D S R D N D H F W E Q Q L D G L D W T A 400
1321 CAAGACATCGTGGCGTTTGGCAAGCACCCAGAGGATGCCAGTCCAGTAATGGTTCT 1380
401 Q D I V A F L A K H P E D V Q S S N G S 420
1381 GTGTACACCTGGAGAGAACGCTTCAACGAGACTAACCCAGGGCAATCCGGACCATATCTCGC 1440
421 V Y T W R E A F N E T N Q A I R T I S R 440
1441 TTCATGGAGTGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC 1500
441 F M E C V N L N K L E P I A T E V W L I 460
1501 AACAAAGTCCATGGAGCTGGATGAGAGGAAGTCTGGCTGGTATTGTGTTCACTGGA 1560
461 N K S M E L L D E R K F W A G I V F T G 480
1561 ATTACTCCAGGCAGCATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1620
481 I T P G S I E L P H H V K Y K I R M D I 500
1621 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGTACTGGGACCTGGCCTCGAGCT 1680
501 D N V E R T N K I K D G Y W D P G P R A 520
1681 GACCCCTTGAGGACATGCGGTACGTGGGGGCTCGCTACTTGCAGGATGTGGTG 1740
521 D P F E D M R Y V W G G F A Y L Q D V V 540
1741 GAGCAGGCAATCATCAGGGTGGTACGGGACCCGAGAAGAAAATGGTGTCTATATGCAA 1800
541 E Q A I I R V L T G T E K K T G V Y M Q 560
1801 CAGATGCCCTATCCCTGTTACGTTACGTGACATCTTCTGCGGGTGTGAGCCGGTCAATG 1860
561 Q M P Y P C Y V D D I F L R V M S R S M 580
1861 CCCCTCTTCATGACGCTGGCCTGGATTACTCAGGGCTGTGATCATCAACGGCATCGT 1920
581 P L F M T L A W I Y S V A V I I K G I V 600
1921 TATGAGAAGGAGGCACGGCTGAAAGAGACCATGGGATCATGGGCTGGACAAACACCAC 1980
601 Y E K E A R L K E T M R I M G L D N S I 620
1981 CTCTGGTTAGCTGGTCATTAGTAGCCTCATTCTCTTGAGGGCTGGCCTGCTA 2040
621 L W F S W F I S S L I P L L V S A G L L 640
2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGTACCCAGCGTGGTGTGTC 2100
641 V V I L K L G N L L P Y S D P S V V F V 660

2101 TTCCCTGTCCGTGTTGCTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTC 2160

661 F L S V F A V V T I L Q C F L I S T L F 680
 2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTCACCGCTGTACCTGCC 2220
 681 S R A N L A A A A C G G I I Y F T L Y L P 700
 2221 TACGTCCTGTGTGGCATGGCAGGACTACGTGGCTTCACACTCAAGATCTTCGCTAGC 2280
 701 Y V L C V A W Q D Y V G F T L K I F A S 720
 2281 CTGCTGTCTCCTGTGGCTTTGGGTTGGCTGTGAGTACTTGCCCTTTGAGGAGCAG 2340
 721 L L S P V A F G F G C E Y F A L F E E Q 740
 2341 GGCATTGGAGTGCAGTGGGACAACCTGTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 2400
 741 G I G V Q W D N L F E S P V E E D G F N 760
 2401 CTCACCACTTCGGTCTCCATGATGCTGTTGACACCTTCCTATGGGGTGTGACCTGG 2460
 761 L T T S V S M M L F D T F L Y G V M T W 780
 2461 TACATTGAGGCTGTCTTCCAGGCCAGTACGGAATTCCCAGGCCCTGGTATTTCCCTGC 2520
 781 Y I E A V F P G Q Y G I P R P W Y F P C 800
 2521 ACCAAGTCCTACTGGTTGGCGAGGAAGTGATGAGAAGAGCCACCCCTGGTCCAACCAG 2580
 801 T K S Y W F G E E S D E K S H P G S N Q 820
 2581 AAGAGAAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTGAGCTGGCGTGTCC 2640
 821 K R I S E I C M E E E P T H L K L G V S 840
 2641 ATTCAAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCGATGCCCTGGCA 2700
 841 I Q N L V K V Y R D G M K V A V D G L A 860
 2701 CTGAATTTTATGAGGGCCAGATCACCTCCTGGCCACAATGGAGCGGGGAAGACG 2760
 861 L N F Y E G Q I T S F L G H N G A G K T 880
 2761 ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCACCGCTACATCCTG 2820
 881 T T M S I L T G L F P P T S G T A Y I L 900
 2821 GGAAAAGACATTGCTCTGAGATGAGCACCCTGGGAGAACCTGGGGTCTGCCCCAG 2880
 901 G K D I R S E M S T I R Q N L G V C P Q 920
 2881 CATAACGTGCTGTTGACATGCTGACTGTCGAAGAACACATCTGGTTCTATGCCCGTTG 2940
 921 H N V L F D M L T V E E H I W F Y A R L 940
 2941 AAAGGGCTCTCTGAGAAGCACCGTGAAGGGAGATGGAGCAGATGCCCTGGATGTTGGT 3000
 941 K G L S E K H V K A E M E Q M A L D V G 960
 3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060
 961 L P S S K L K S K T S Q L S G G M Q R K 980
 3061 CTATCTGTGGCCTTGGCCTTGTGGGGATCTAAGGTGTCATTCTGGATGAACCCACA 3120
 981 L S V A L A F V G G S K V V I L D E P T 1000
 3121 GCTGGTGTGGACCCCTACTCCCGCAGGGAAATATGGAGCTGCTGCTGAAATACCGACAA 3180
 1001 A G V D P Y S R R G I W E L L L K Y R Q 1020
 3181 GGCCGCACCATTATTCTCTACACACCACATGGATGAAGCGGACGTGCTGGGGACAGG 3240
 1021 G R T I I L S T H H M D E A D V L G D R 1040
 3241 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGGCTCCCTGTTCTGAAGAAC 3300
 1041 I A I I S H G K L C C V G S S L F L K N 1060
 3301 CAGCTGGGAACAGGCTACTACCTGACCTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360

1061 Q L G T G Y Y L T L V K K D V E S S L S 1080
 3361 TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCAG 3420
 1081 S C R N S S S T V S Y L K K E D S V S Q 1100
 3421 AGCAGTTCTGATGCTGGCCTGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
 1101 S S S D A G L G S D H E S D T L T I D V 1120
 3481 TCTGCTATCTCAAACCTCATCAGGAAGCATGTGTCAGGCCGGCTGGTGGAAAGACATA 3540
 1121 S A I S N L I R K H V S E A R L V E D I 1140
 3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTGTGGAA 3600
 1141 G H E L T Y V L P Y E A A K E G A F V E 1160
 3601 CTCTTCATGAGATTGATGACCGGCTCTCAGACCTGGCATTCTAGTTATGGCATCTCA 3660
 1161 L F H E I D D R L S D L G I S S Y G I S 1180
 3661 GAGACGACCCCTGGAAGAAATATTCTCAAGGTGGCGAAGAGACTGGGTGGATGCTGAG 3720
 1181 E T T L E E I F L K V A E E S G V D A E 1200
 3721 ACCTCAGATGGTACCTGCCAGCAAGACGAAACAGGCAGGCCCTCGGGGACAAGCAGAGC 3780
 1201 T S D G T L P A R R N R R A F G D K Q S 1220
 3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA 3840
 1221 C L R P F T E D D A A D P N D S D I D P 1240
 3841 GAATCCAGAGAGACAGACTTGCTCAGTGGATGGATGGCAAAGGGCCTACCAAGGTGAAA 3900
 1241 E S R E T D L L S G M D G K G S Y Q V K 1260
 3901 GGCTGGAAACTTACACAGCAACAGTTGTGGCCCTTTGTGGAAGAGACTGCTAATTGCC 3960
 1261 G W K L T Q Q Q F V A L L W K R L L I A 1280
 3961 AGACGGAGTCGAAAGGATTTTGCTCAGATTGCTTGCAGCTGTGTTGTCTGCATT 4020
 1281 R R S R K G F F A Q I V L P A V F V C I 1300
 4021 GCCCTTGTGTTCAGCCTGATCGTGCCACCCCTTGCAAGTACCCCAGCCTGGAACCTCAG 4080
 1301 A L V F S L I V P P F G K Y P S L E L Q 1320
 4081 CCCTGGATGTACAACGAACAGTACACATTGTCAGCAATGATGCTCCTGAGGACACGGGA 4140
 1321 P W M Y N E Q Y T F V S N D A P E D T G 1340
 4141 ACCCTGGAACCTTAAACGCCCTCACCAAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA 4200
 1341 T L E L L N A L T K D P G F G T R C M E 1360
 4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGAGGAAGAGTGGACCAACTGCCCA 4260
 1361 G N P I P D T P C Q A G E E E W T T A P 1380
 4261 GTTCCCCAGACCATCATGGACCTCTTCCAGAACATGGAACTGGACAATGCCAGAACCCCTCA 4320
 1381 V P Q T I M D L F Q N G N W T M Q N P S 1400
 4321 CCTGCATGCCAGTGTAGCAGCGACAAATCAAGAAGATGCTGCCCTGTGTCAGGACCTG 4380
 1401 P A C Q C S S D K I K K M L P V C P P G 1420
 4381 GCAGGGGGCTGCCCTCCACAAAGAAAACACTGCAGATATCCTTCAGGACCTG 4440
 1421 A G G L P P P Q R K Q N T A D I L Q D L 1440
 4441 ACAGGAAGAAACATTCGGATTATCTGGTAAGACGTATGTGCAAGATCATAGCCAAAGC 4500
 1441 T G R N I S D Y L V K T Y V Q I I A K S 1460
 4501 TTAAAGAACAGATCTGGGTGAATGAGTTAGGTATGGCGGCTTTCCCTGGGTGTCAGT 4560

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1461 L K N K I W V N E F R Y G G F S L G V S 1480
4561 AATACTCAAGCACTTCCGCCAGTCAGAAGTTAACATGATGCCACAAACAAATGAAGAAA 4620
1481 N T Q A L P P S Q E V N D A T K Q M K K 1500
4621 CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTT 4680
1501 H L K L A K D S S A D R F L N S L G R F 1520
4681 ATGACAGGACTGGACACCAGAAATAATGTCAGGTGTGGTTCAATAACAAGGGCTGGCAT 4770
1521 M T G L D T R N N V K V W F N N K G W H 1540
4741 GCAATCAGCTCTTCCTGAATGTCATCAACAATGCCATTCTCCGGCCAACCTGCAAAG 4800
1541 A I S S F L N V I N N A I L R A N L Q K 1560
4801 GGAGAGAACCTAGCCATTATGGAATTACTGCTTCATCCCCCTGAATCTCACCAAG 4860
1561 G E N P S H Y G I T A F N H P L N L T K 1580
4861 CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTGTGTCCATCTGT 4920
1581 Q Q L S E V A P M T T S V D V L V S I C 1600
4921 GTCATCTTGCAATGTCCTCGTCCCAGCCAGCTTGTGTATTCCGTATCCAGGAGCGG 4980
1601 V I F A M S F V P A S F V V F L I Q E R 1620
4981 GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5040
1621 V S K A K H L Q F I S G V K P V I Y W L 1640
5041 TCTAATTTGTCTGGATATGTGCAATTACGTTGTCCTGCCACACTGGTCATTATCATC 5100
1641 S N F V W D M C N Y V V P A T L V I I I 1660
5101 TTCACTGCTTCCAGCAGAAGTCCTATGTCCTCCACCAATCTGCCTGTGCTAGCCCTT 5160
1661 F I C F Q Q K S Y V S S T N L P V L A L 1680
5161 CTACTTTGCTGTATGGTGGTCAATCACACCTCTCATGTACCCAGCCTCTTGTTGTT 5220
1681 L L L Y G W S I T P L M Y P A S F V F 1700
5221 AAGATCCCCAGCACAGCCTATGTTGGTGTCAACAGCGTGAACCTCTTCATTGGCATTAAAT 5280
1701 K I P S T A Y V V L T S V N L F I G I N 1720
5281 GGCAGCGTGGCCACCTTGTGCTGGAGCTGTTCACCGACAATAAGCTGAATAATATCAAT 5340
1721 G S V A T F V L E L F T D N K L N N I N 1740
5341 GATATCCTGAAGTCCGTGTTCTGATCTCCCACATTTGCCTGGACGAGGGCTCATC 5400
1741 D I L K S V F L I F P H F C L G R G L I 1760
5401 GACATGGTAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTGGGAGAATCGCTTT 5460
1761 D M V K N Q A M A D A L E R F G E N R F 1780
5461 GTGTCACCATTATCTGGACTTGGTGGACGAAACCTCTGCCTGGCGTGGAAAGGG 5520
1781 V S P L S W D L V G R N L F A M A V E G 1800
5521 GTGGTGTCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT 5580
1801 V V F F L I T V L I Q Y R F F I R P R P 1820
5581 GTAAATGCAAAGCTATCCTCTGAATGATGAAGATGAAGATGTGAGGGGGAAAGACAG 5640
1821 V N A K L S P L N D E D E D V R R E R Q 1840
5641 AGAATTCTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700
1841 R I L D G G G Q N D I L E I K E L T K I 1860
5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTGCGTGGCATTCCCTGGTGAG 5760

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1861 Y R R K R K P A V D R I C V G I P P G E 1880
 5761 TGCTTGCGCTCCTGGAGTTAATGGGCTGGAAAATCATCAA
CTTCAAGATGTTAAC 5820
 1881 C F G L L G V N G A G K S S T F K M L T 1900
 5821 GGAGATACCACTGTTACCAAGAGGAGATGCTTCCTAACAGAA
ATAGTATCTTATCAAAC 5880
 1901 G D T T V T R G D A F L N R N S I L S N 1920
 5881 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTGATGCC
CATCACAGAGCTG 5940
 1921 I H E V H Q N M G Y C P Q F D A I T E L 1940
 5941 TTGACTGGAGAGAACACGTGGAGTTCTTGCCCTTGAGAGGAGTCCC
AGAGAAAAGAA 6000
 1941 L T G R E H V E F F A L L R G V P E K E 1960
 6001 GTTGGCAAGGTTGGTGAATGGCGATTGGAAACTGGGCCTCGTGAAGTATGGAGAAAAA 6060
 1961 V G K V G E W A I R K L G L V K Y G E K 1980
 6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCT
TACAGCCATGGCTTGATC 6120
 1981 Y A G N Y S G G N K R K L S T A M A L I 2000
 6121 GGCGGGCCCTCTGTGGTGTGATGAACCCACCACAGGCATGGAT
CCCCAAAGCCCCGG 6180
 2001 G G P P V V F L D E P T T G M D P K A R 2020
 6181 CGGTTCTTGTGGAATTGTGCCCTAACGTGTTGTCAAGGAGGGAGATCAGTAGTGCTTACA 6240
 2021 R F L W N C A L S V V K E G R S V V L T 2040
 6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTGCACTAGGATGGCAAT
CATGGTCAATGGA 6300
 2041 S H S M E E C E A L C T R M A I M V N G 2060
 6301 ACAGTTCAAGGTGCCCTGGCAGTGTCCAGCATCTAAAAAA
TAGGTTGGAGATGGTTATACA 6360
 2061 R F R C L G S V Q H L K N R F G D G Y T 2080
 6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATT
TTGGGA 6420
 2081 I V V R I A G S N P D L K P V Q D F F G 2100
 6421 CTTGCATTCCCTGGAAGTGTCCAAAAGAGAAACACCGGAACATGCTACA
ATACCAAGCTT 6480
 2101 L A F P G S V P K E K H R N M L Q Y Q L 2120
 6481 CCATCTTCATTATCTCTGCCAGGATATTCA
GCATCCTCTCCCAGAGCAAAAGCGA 6540
 2121 P S S L S S L A R I F S I L S Q S K K R 2140
 6541 CTCCACATAGAAGACTACTGTGTTCTCAGACA
ACACTGACCAAGTATTGTGAACTTT 6600
 2141 L H I E D Y S V S Q T T L D Q V F V N F 2160
 6601 GCCAAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATTACAC
AAAAACCAGACA 6660
 2161 A K D Q S D D D H L K D L S L H K N Q T 2180
 6661 GTAGTGGACGTTGCAGTTCTCACATCTTCTACAGGATGAGAA
AGTGAAGAAAGCTAT 6720
 2181 V V D V A V L T S F L Q D E K V K E S Y 2200
 6721 GTATGAAGAATCCTGTTCATACGGGGTGGCTGAAAGTAA
AGAGGGACTAGACTTTCTTT 6780
 2201 V *
 6781 GCACCATGTGAAGTGTGAGAAAAGAGCCAGAAGTTGATGTGG
AAGAAGTAAACTG 6840
 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880

Figure 3

5' 1 GTACCCCCCT TGCCTGGTTG ATCCTCAGGG TTCTACTTAG AATGCCTCGA

51 AAAGTCTTGG CTGGACACCC ATGCCAGTC TTTCTGCAGG GTCCCATTGG
101 GGTAAACCTT CTCATTCAT CCCATGTGAA CCAGGCCAGG CCCATCAGGG
151 TTTGGCAACC CCCTGATGCA GTGGTTGCTG CCAGGTGACA GGAGCAAGCC
201 TGCACTGCT GGGGGCCAT GCAGAGACAG CCTGCCAGAG GGGAGACCAC
251 CTGGGGAGGC CAGAGCCGTG GAGACAGCAA GAGACCAGGG GCTGAGGACA
301 GAGTAGTACA GGTCTTGTT CCCAGTAGTC CTGAAACCAC TGCACTCCGA
351 ACCTTTCTGT ACTTAGCTTA AGCCAGTTGG AGTTTCTGTC CTTTACAACC
401 AAGAGCCTTG ATAGGAATGG GGTCTGTGC TACGCTACTG TTGGCTTCTT
451 TCCCGATCGG GCGCTGGAGG GGAACACAGC AGTCACTACA GTGGGATGCT
501 TACTCGGTGC TGGGCATGCT AGAAAAGTGC TGCCATGCCT TATTCCCAC
551 GTGGTGGGGA TTTTGACCCC ACCTGTACAG ACAGATAAGT GAGGACCCCTT
601 TTCACCTTAT CCTGCAACAG AAAATCCAGC AGCCAAAGCC AACAAAGGCC
651 CAGCATAGCA TCTTCCCTCT CTGACTTCAT CCTCACGCTC CACACACCAC
701 CCCCCCTGGCC ATTCCCAGCA GCCCAGTAAG CACTGCCTCA CACTTCCAGT
751 TCCGGACCAG CCAGGATGGC CAGGCTGGAT GGGGGCCATC CACCGGCTGA
801 AGCCAATTGC CTATTCTCGA GCTGAAGGTG AATCAATCCC GCATAAATCT
851 TCGGGCAGAG AACTNGGGTG GGGGGTAGAA GAGGGGAAAT GTCTAGAAGG
901 AAATTCTGGG GCACATTCCCT GGAAGTGAGG AGGATGGATA TTGGACAGAA
951 ATTATGTCA TGCAGGCACC CTCACTTGCC CTGGCCACAT GGACAGTTCC
1001 TCCCCGGCTG TGTTCCGNNGC CTCCCTCTCGT GCTCCAGGGC CTGTCTGTTC
1051 CTGGAGCGAG ATGGGTCCCA GGGCTGGCA CCAGTCCCCA TCTCCAGCCA
1101 TCAGGCACCTT TCCTCTCTGT GTTTTGGCGT AAACACNTCC CTAGGTTTGT
1151 GGATCTGAAT CCTCTTCCCA ACACACTCAA GCTTGCTGG GCCTCCCTGC
1201 AGTGTATGTT TAAGGCACCA CACAGCCTCC AAGGCCTGGC ACCCGGGCAG
1251 TGGCCACCTG GTAAACACAG CAGTCAGATT TCCTCATTTC AGCCAAGTGT
1301 AAAATCAAGG TAATGGATCT ACNCTTTTT TTTNTNTTT TTTCCAGGGG
1351 GNTNNNTTTT TTTTGAGACG GAGTCTCACT CTGTCANCCC CGGTCTGGAG
1401 TGCAGTGGCT CAATCTCGGC TCANCTGGCA AGCTCCGCCT CCCAGTTCA
1451 TGCCATTCTC CTGCCTCAGC CTACATAGTA GCTGGGACTA CAGGTGCCCG
1501 CCACCACACC TAGCTAATT TTTGTATTT TAGTAGAGAC GGGGTTTCAT
1551 CATGTTAGCC AGGATGGTCT CGATCTCTG ACCTCCAAA GTGGTGGGAG
1601 TTACAGGTGT GAGCCACTGC GCNCCGGCTG GATGACTCTT GAGACAACAC
1651 CATTCAAGACA AAGGCAAGGC CTCCCCACTTA AACTCATAAC CGTGTCTCCT
1701 TTCTCTCCTT CGATTGAGC GGCTGAATT GGTTACAGTC ATCTGACCTG
1751 TGGGTGTGAA NGTCCACCTG CCTGGCATAA AAAGCTGTGC CTCCCTTCTA
1801 GGTGAGGAGA AAGAGAGAGA CCTGGCTCAT CTGAGGTGTG GTTGGGAGGG
1851 GGGACCCAGG TGTGCTGGAA ATGAAAAGAA ATGCATTCCCT GTTTTTCGT
1901 CCCAACATGC AAACAACGTGA ACAAAAGCAT TAGGGCCTGA GACTGGGAGT
1951 AAAGAATTCC TTGTCAACCAT GGATACCAGG AAATGGCCCC ACTTATATAT
2001 AATAAGGGCT TTAGAGATGC TGGACCATCT GATATTCCAG CCTGGGGCCA
2051 CATGGGAGTG TGCCCTGGTG TTATTCCCTA TACAGTTCCA TGAACATGGC
2101 TCTGGAAACA CCTCTGTCTG CAGAAAATGA GGCTTTCTT TTTTTGTTCG

2151 GGGGTGAACA GAGGGCAGAG GCCTGGGCAT CTTCACTCAG CACCCCTTG
 2201 TAACCCAGCA CTTAGCACCA TGGCTGGCGC ACAGCAATGT CACATGTG
 2251 AGTGCACACG ATGCCCACT GCCAGGGTC ACCCCACACC GGTGCTGTTG
 2301 GGGCGTTGG AGTGGTTATC TCTTCTTAG TCCTCAAGCT CCTACCTGGC
 2351 AGAGAGCTGC CCAACACCGT CGGGGTGGGG TGGGCGGGAA GGGAAAGAAC
 2401 AGCAGCAAGA AAGAAGCCCC CTGGCCCTCA CTCTCCCTCC CTGGACGCC
 2451 CCTCTTCGAC CCCATCACAC AGCCGCTTGA GCCTTGGAGN CAGTGGATT
 2501 CCGAGCCTGG GAACCCCCGG CGTCTGTCCC GGTGTCGGGG GCAGCCTCAC
 2551 CCNCGTGCTG GCCCAGCCCC CGCGAGTTCG GGACCCGGGG TTTCCGGGT
 2601 GGCAGGGGGT TCCCATGCCG CCTGCGAGGC CTCGGCTCGG GCGCTCCCG
 2651 GAACCTGCAC TTCAGGGTC CTGGTCCGCC GCCCCCAGCA GGAGCAAAAC
 2701 AAGAGCACGC GCACCTGCCG GCCCGCCCGC CCCCTTGGTG CCGGCAATC
 2751 GCGCGCTCGG GGCGGGTCG GGCGCGCTGG AACCAAGAGCC GGAGCCGGAT
 2801 CCCAGCCGGA GCCCAAGCGC AGCCCGCACC CGCGCAGCG GCTGAGCCGG
 2851 GAGCCAGCGC AGCCTCGGCC CGCAGCTCA AGCCTCGTCC CCGCCGCCNG
 2901 CCGCCGCACG CCGCCGCCGC CGCCCCCGGG GCATGGCTGT CTGATGCCG

EXON1/INTRON 1

2951 CTTTCTCGGT CGGCACCGCC ATGGTGAGTG AGCGCATCCT TCGTCCGCCG
 3001 GGAAACGGTTT TATTTCAAG GAGAGCAGGA AACACACAAA GACTCGCAAG
 3051 CTCGACCTGA CACCCCTCCC AGGAGCGCGT CCTCTGGGGC GCTGACCCAG
 3101 GGGCACCCCTA GAGTGGCGCC CGGCTCCGAT CGCTGCCCT NNCCCCCTCG
 3151 CCAGGGCCAC CTGGGAGCCT CGGGGATGCC CCTTGCACCG GCAGAGNGCA
 3201 CGGACTAGGT GGAGGGGNCC GGGATTGGGG CGGGGGGCAG NCAGTTGCC
 3251 TACAAGTTGG ACCGATGGCC TTGACCTGAT GGCTCTGGG CGGGGGCGT
 3301 GGGGAGCTGG GGACCCGGAG CGCACTGGGG ACTGGGGAGG GGCGCAGCT
 3351 TGGGCCGGAG GGAAGAGGGG ACTTGAAGAA GGGGAGCCCC GCGCGCGCG
 3401 CTGTGGGCTT GGGGACCGGG GACTTCTCGC GCCATCCCCA GGAACCCAG
 3451 GCAAGGTCTG GGGAACAAAA GAGGAAGCTG CCCCCAGAGA GCCGGAGCTC
 3501 GACTGNACTC CC 3'

Figure 4

5'

1 CTTGGTGCCG CATGCATCGT GGTGCTCATC TTTCTGGCCT TCCAGCAGAG
 51 GGCATATGTG GCCCCTGCCA ACCTGCCCTGC TCTCCTGCTG TTGCTACTAC
 101 TGTATGGCTG GTGATCACCA CCGCTCATGT ACCCAGCCTC CTTCTTCTTC
 151 TCCGTGCCCA GCACAGCCTA TGTGGTGCTC ACCTGCATAA ACCTCTTTAT
 201 TGGCATCAAT GGAAGCATGG CCACCTTGT GCTTGAGCTC TTCTCTGATC
 251 AGAAGCTGCA GGAGGTGAGC CGGATCTTGA AACAGGTCTT CCTTATCTTC
 301 CCCACTTCTG CTTGGGCCGG GGGCTTATTG ACATGGTGCG GNAACCAGGC
 351 CATGGCTGAT GCCTTGANC CCTTGGAAA AAGGCAGTTC AAGTACCTG

401 NCTTGGAAAGG TGGCGGAAGA ACCTTTGGC ATGGGAACAG GGCCCCTTT
451 CCTTCTCTTC ACACTANTGT TCAAGCACCG AAGCCAACTC NTGCCACAAG
501 CCCAGGTAAAG GTCTCTGCCA CTCCTGGAGA GAGACGAGGA TGTAGCCCGT
551 GAACGGGAGC GGGTGGTCCA AGGAGCCACC CAGGGGGATG TGTGGTGCT
601 GAGGAACCTG ACCAAGGTAT ACCGTGGCA GAGGATGCCA GCTGTTGACC
651 GCTTGTGCCT GGGGATTCCC CCTGGTGAGT GTTTGGGCT GCTGGGTGTG
701 AACGGAGCAG GGAAGACGTC CACGTTCGC ATGGTGACGG GGGACACATT
751 GGCCAGCAGG GGCAGGGCTG TGCTGGCAGG CCACAGCGGG CCCGGGAACC
801 CAGTGTGCGC ACCTCNAGGG CAGGCNCAGC GTGGCCCGGG AACCCAGTGC
851 TGCGCACCTA AGCATGGGAT ACTGCCCTNA ATCCGATGCC ATCTTGAGC
901 TGCTGACGGG CCGCGAGCAC CTGGAGCTGC TTGCGCCCT GCGCGGTGTC
951 CCGGAGGCCA AGGTTGCCA NACCGNTGGC TCGGGCCTGG CGCGTCTGGG
1001 ACTCTCATGG TACGCAGACC GGCCTGCAGG CACCTACAGG AACCTGCCCG
1051 GGCGGCCGCT CGAGCCNTA NNTGAAGTA 3'

Figure 4b

...CTCCTGCCAC AGTTAGTGAG GTCTATGGAG AGGGTGGCAG GGGCCAAGGA
CCTACTTTAA GCCCACAGAT ATTCTGTCCC CAGGCCAGG GTGAGGTCTC...

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Figure 5

CDNA-sequences of lipid sensitive Genes:

ABCB9, ABCA6, ABCC4, ABCA1, ABCD2, ABCB1, ABCB4, ABCC2, ABCD1, ABCC1, ABCB6, ABCB11, ABCG2, ABCC5, ABCA5, ABCG1, ABCA3

ABCB9 GENBANK:U66676

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GGAACCCCCCAGTCCTCATCCTGGATGAAGGCCAACAGCGCTTGGATGCCGAGAGCGAGT
ATCTGATCCAGCAGGCCATCCATGGCAACCTGTCAAGAACACAGGTACTCATCATCGCG
CACCGGCTGAGCACCAGTGAGCACCGCACCTCATTGTGGTGTGGACAAGGGCCCGTA
GTGCAGCAGGGCACCCACCAGCAGCTTGCTTGCCTCAGGGCGGGCTTTACGGCAAGCTN
GTTGCAGCGGAGATGTGGGTTCAAGGCCAGACTTCACAGCTGCCACAACGAGCC
TGTAGCCAACGGGTACAAGGCCTGATGGGGGCCCTCCTCGCCCGGTGGCAGAGGAC
CCGGTGCCTGCCTGGCAGATGTGCCAACGGAGGTTCCAGCTGCCCTACCGAGCCCAGGC
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ABCC4 GENBANK: U66682

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ABCA1 Acc. Nr.: AJ012376 GENBANK: HSA012376

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ABCD2 Acc.Nr.: AJ000327 GENBANK: HSALDR

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AAAAAAA

ABCB1 Acc. Nr. M14758 GENBANK: HUMMDR1

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ABCB4 Acc. Nr.: M23234 GENBANK: HUMMDR3

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ABCC2 Acc.Nr.: U49248 GENBANK: HSU49248

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ABCA5 Acc. Nr. : AF000148 GENBANK:HSAF000148

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 TGCTGGGTCTTAGCGTCCAGCGCAGCCCCGGGGCATCCTGGAGGCTCTGCTCCCTTAGG
 GCATGGTAGTCACCGCGAAGCCGGCACCGTCCCACAGCATCTCCAGAACAGCCGGCA
 CAGGAGGGAAAGGTGCCAGGCTCGAACGAGCTCTGTTCCAGCACTGCACCCTCAGGAA
 GTCGCCCGCCCCAGGACACGCAGGGACCACCTAACGGCTGGGTGGCTGTCTAAGGACA
 CATTGAATACGTTGTGACCATCCAGAAAATAATGCTGAGGGACACAAAAAAAAAAAA
 AAAAAAAAAA

Fragment 640918

1 GAGATCCTGAGGTTTCCCCAGGCTGCTCAGCAGGAAGGTTCTCCTCCCTGATGGTC
 61 TATAAGTTGCCTGTTGAGGATGTGCGACCTTATCACAGGCTTCTTCAAATTAGAGATA
 121 GTTAAACAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTACCCCTGGAGCAGGTT
 181 TTCCTGGAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTGAAGAGGACTTGTGATCCCTCG
 241 GTGAAGTGGAAACTCCTCCTGCAGGAAGAGCCTAACAGCTCCAAATACCCCTATATCTTC
 301 TTTAATCCTGTGACTTTAAAGATAATATTTATAGCCTTAATATGCCTTATATCAGA
 361 GGTGGTACAAATGCATTTGAAACTCATGCAATAATTATC

Fragment 698739

1 GCTCTCACACAGAGATTTGAAGCTTTCCCACAGGCTGCTGGCAGGAAGATATTCC
 61 TCTTTAATGGCGTATAAGTTACCTGTGGAGGATGTCCACCCCTATCTCGGGCCTTTTC
 121 AAGTTAGAGGCATGAAACAGACCTCAACCTGGAGGAATACAGCCTCTCAGGCTACC
 181 TTGGAGCAGGTATTCTAGAACTCTGTAAAGAGCAGGAGCTGGAAATGTTGATGATAAA
 241 ATTGATACAACAGTGAATGAAACTCTCCCACAGGAAGACCCCTAACATGAAGAACCT
 301 CCTAACATTCAATTAGTCCTACTACATTGTTAGTTCCATAATTCTACAAGAATGTT
 361 TCCTTTACTTCAGTTAACAAAAGAAAATTTAAATAAACATTCAATAATGATTACAGTT
 421 TTCATTTAAAATTTAGGATGAAGGAAACAAGGAAATATAGGAAAAGTAGTAGACAA
 481 AATTAACAAAATCAGACATGTTATTCACTCCCCAACATGGGTCTATTTGTGCTAAAAAT
 541 AATTAAAAATCATACAATATTAGGTTGGTTATCG

Fragment 990006

1 GTGGAAGATGTGCAACCTTACGCCAAGCTTCTCAAATTAGAGAAGGTTAACAGAGC
 61 TTTGACCTAGAGGAGTACAGCCTCTCACAGTCTACCCCTGGAGCAGGTTCTGGAGCTC
 121 TCCAAGGAGCAGGAGCTGGGTGATTTGAGGAGGATTTGATCCCTCAGTGAAGTGGAAAG

181 CTCCTCCCCAGGAAGAGCCTTAAAACCCAAATTCTGTGTTCTGTTAAACCCGTGGT
 241 TTTTTTAAATACATTATTTTATAGCAGCAATGTTCTATTAGAAACTATATTATA

Fragment 1133530

1 TTTCAGTTG CATGTAATAC CAAGAAATCG AATTGTTTC CGGTTCTTAT
 51 GGGAATTGTT AGCAATGCC TTATTGGAAT TTTAACCTTC ACAGAGCTTA
 101 TTCAAATGGA GAGCACCTTA TTTTTCTGTG ATGACATAGT GCTGGATCTT
 151 GGTTTTATAG ATGGGTCCAT ATTTTGTTG TTGATCACAA ACTGCATTTC
 201 TCCTTATATT GGCATAAGCA GCATCAGTGA TTATT

Fragment 1125168

CTGGATT

TGCTCTGC GG CAAGACCCGC GCCACCAGCG GCAGTATCCA GTTCGACGGC
 CAGGAAC TGA CCAAAATGCG CGAATACAAC ATCGTGC GGG CGGGGTAGG
 GCGCAAGTTT CAGAACCCGT CGATCTACGA AAACCTCACG GTGTTTGAAA
 ACCTTGAGAT GTCTTATCCG GCTGGCGCA AGGTCTGGG TGCGCTGTTT
 TTCAAGCGCA ATGCCAGGT GGTGGCGCGG GTCGAG

Fragment 1203215

1 ATCGCCGATA TCTCCCCTTC GGGCTGC GG AAGAGCACCT TCCTGAAAGT
 51 GCTCGCCGGG TTCTATGCC TGGACACCGG GCGCTTCAGG ATCAACGGCC
 101 AGGCGATGCG GCATTTCGGT TTGCGCTCGT ACCGCCAGAG CGTGGCCTAT
 151 GTCACGGCCC ACGACGAGAT CATGCCGGG ACGGTGATCG AGAACATCCT
 201 GATGGACAGC GACCCGCTGG ACGGCACGGG TTTGCAGAGC TGTGTCGAGC
 251 AGGCCGGGTT GCTGGAAAGC ATCCTGAAAC TGAGCAATGG CTTCAATACC
 301 TTGCTCGGAC CCATGGCGT GCAATTGTCC TCGGGCCAGA AGCAACGCCT
 351 GTTGATCGCC CGGGGTGAC GC

Fragment 168043

1 AAAACCAAAG ATTCTCCTGG AGTTTCTCT AAACTGGGTG TTCTCCTGAG
 51 GAGAGTTGAC AAGAAACTTG GTGAGAAATA AGCTGGCAGT GATTACGCGT
 101 CTCCTTCAGA ATCTGATCAT GGGTTGTTTC CTCTTCTCTC TCGTTCTGCG
 151 GGTCCGAAGC AATGTGCTAA AGGGTGCTAT CCAGGACCGC GTAGGTCTCC
 201 TTTACCAGTT TGTGGCGCC ACCCGTACA CAGGCATGCT GAACGCTGTG
 251 AATCTGTTTC CCGTGCTGCG AGCTGTCAGC A

Huwhite2

1 ATGGCCGTGA CGCTGGAGGA CGGGGCGGAA CCCCCTGTGC TGACCACGCA
 51 CCTGAAGAAG GTGGAGAACCC ACATCACTGA AGCCCAGCGC TTCTCCCACC
 101 TGCCCAAGCG CTCAGCCGTG GACATCGAGT TCGTGGAGCT GTCCTATTCC
 151 GTGCAGGGAGG GCCCCTGCTG GCGCAAAGG GGTTATAAGA CCCTTCTCAA
 201 GTGCCTCTCA GGTAAATTCT GCCGCCGGGA GCTGATTGGC ATCATGGGCC
 251 CCTCAGGGGC TGGCAAGTCT ACATTCACTGA ACATCTTGGC AGGATACAGG
 301 GAGTCTGGAA TGAAGGGCA GATCCTGGTT AATGGAAGGC CACGGGAGCT

351 GAGGACCTTC CGCAAGATGT CCTGCTACAT CATGCAAGAT GACATGCTGC
401 TGCCGCACCT CACGGTGTG GAAGCCATGA TGGTCTCTGC TAACCTGAAT
451 CTTACTGAGA ATCCCGATGT GAAAAACGAT CTCGTGACAG AGATCCTGAC
501 GGCACGGGGC CTGATGTCGT GCTCCCACAC GAGGACAGCC CTGCTCTTG
551 GCGGGCAGAG GAAGCGTCTG GCCATCGCCC TGGAGCTGGT CAACAACCCG
601 CCTGTCATGT TCTTGATGA GCCCACCAGT GGTCTGGATA GCGCCTCTTG
651 TTTCCAAGTG GTGTCCTCA TGAAGTCCCT GGCACAGGGG GGCGTACCA
701 TCATCTGCAC CATCCACCAG CCCAGTGCCA AGCTCTTGA GATGTTGAC
751 AAGCTCTACA TCCTGAGCCA GGGTCAGTGC ATCTTCAAAG GCGTGGTCAC
801 CAACCTGATC CCCTATCTAA AGGGACTCGG CTTGCATTGC CCCACCTACC
851 ACAACCCGGC TGACTTCAGT GAGTGGGGT CTGTTGCCTC TGGCGAGTAT
901 GGACACCTGA ACCCCATGTT GTTCAGGGCT GTGCAGAAATG GGCTGTGCGC
951 TATGGCTGAG AAGAAGAGCA GCCCTGAGAA GAACGAGGTC CCTGCCCAT
1001 GCCCTCCTTG TCCTCCGGAA GTGGATCCA TTGAAAGCCA CACCTTGCC
1051 ACCAGCACCC TCACACAGTT CTGCATCCTC TTCAAGAGGA CCTTCCTGTC
1101 CATCCTCAGG GACACGGTCC TGACCCACCT ACAGGTTCATG TCCCACGTGG
1151 TTATTGGCGT GCTCATCGGC CTCCTCTACC TGCAATATTGG CGACGATGCC
1201 AGCAAGGTCT TCAACAAACAC CGGCTGCCTC TTCTCTCCA TGCTGTTCC
1251 CATGTTGCC GCCCTCATGC CAACTGTGCT CACCTTCCCC TTAGAGATGG
1301 CGGTCTTCAT GAGGGAGCAC CTCAACTACT GGTACAGCCT CAAAGCGTAT
1351 TACCTGGCCA AGACCATGGC TGACGGTCCC TTTCAGGTGG TGTGTCCGGT
1401 GGTCTACTGC AGCATTGTGT ACTGGATGAA CGGCCAGCCC GCTGAGACCA
1451 GCCGCTTCCT GCTCTTCTCA GCCCTGGCCA CCGCCACCGC CTTGGTGGCC
1501 CAATCTTGG GGCTGCTGAT CGGAGCTGCT TCCAACTCCC TACAGGTGGC
1551 CACTTTGTG GGCCCAGTTA CCGCCATCCC TGTCTCTTG TTCTCCGGCT
1601 TCTTGTCAAGACC ATCCCCACTT ACCTGCAATG GAGCTCCTAT
1651 CTCTCCTATG TCAGGTATGG CTTTGAGGGT GTGATCCTGA CGATCTATGG
1701 CATGGAGCGA GGAGACCTGA CATGTTAGA GGAACGCTGC CGGTTCCGGG
1751 AGCCACAGAG CATCCTCCGA GCGCTGGATG TGGAGGATGC CAAAGCTCTAC
1801 ATGGACTTCC TGGTCTTGGG CATCTTCTTC CTAGCCCTGC GGCTGCTGGC
1851 CTACCTTGTG CTGCGTTACC GGGTCAAGTC AGAGAGATAG AGGCTTGGCC
1901 CAGCCTGTAC CCCAGCCCC GCAGCAGGAA GCCCCCAGTC CCAGCCCTTT
1951 GGGACTGTTT TANCTCTATA CACTTGGCA CTGGTTCTG GCGGGGCTAT
2001 CCTCTCCTCC CTTGGCTCCT CCACAGGCTG GCTGTCGGAC TCGCCTCCCA
2051 GCCTGGGCTC TGGGACTGGG GGCTCCAACC CTCCCCACTA TGCCCAGGAG
2101 TCTTCCCAAG TTGATGCGGT TTGTAGCTTC CTCCCTACTC TCTCCAACAC
2151 CTGCATGCAA AGACTACTGG GAGGCTGCTG CCTCCTCCT GCCCATGGCA
2201 CCCTCCTCTG CTGTCTGCCT GGGAGCCCTA GGCTCTCTAT GGCCCCACTT
2251 ACAACTGA

Fragment 20237

1 TTTAAGGATT TCAGCCTTTC CATTCCGTCA GGATCTGTCA CGGCAC TGCCCAAGT
61 GGTTCTGGCA AATCAACAGT GCTTCACTC CTGCTGAGGT TGTACGACCC TGCTTCTGGA
121 ACTATTAGTC TTGATGCCA TGACAATCCG TCAGCTAAAC CCAGTGTGTG GCTGAGATCC
181 AAAATTGGGA CAGTCAGTCA GGAACCCATT TTGTTTCTT GCTCTATTGC TGAGAACATT
241 GCTTATGGTG CTGATGACCC TTCCTCTGTG ACCGCTGAGG AAATCCAGAG AGTGGCTGAA
301 GTGGCCAATG CAGTGGCTTC TCCGGAATTT CCCCCAAGGT TCAACACTGT GGTTGGAGAA
361 AAGGGTGTTC TCCTCTCAGG TGGGCAGAAA CAGCGGATTG CGATTGCCCG TGCTCTGCTA
421 AAGAACCCCA AAATTCTTCT CCTAGATGAA GCAACCAGTG CGCTGGATGC CGAAAATGAG
481 TACCTTGTTC AAGAACGCTCT AGATGCCCTG ATGGATGGAA GAACGGTGT AGTTATTGCC
541 CATAGCCTGT CCACCATTA GAATGCTAAT ATGGTTGCTG TTCTTGACCA AGGAAAAATT
601 ACTGAATATG GAAAACATGA AGAGCTGCTT TCAAAACCAA ATGGGATATA CAGAAAACCA
661 ATGAACAAAC AAAGTTTTAT TTCAGCATAA GGAAGCAATT ACTGGTAAAC AATATGAGAC
721 TTTAATGCAA AACAGTGTG CGAAAAAAA CTCAGAGACT ATGAAATACA TAAACCATAT
781 ATCAAGTTAT TTGAAAAATA CCTATTTT CCAAAGTGTG

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